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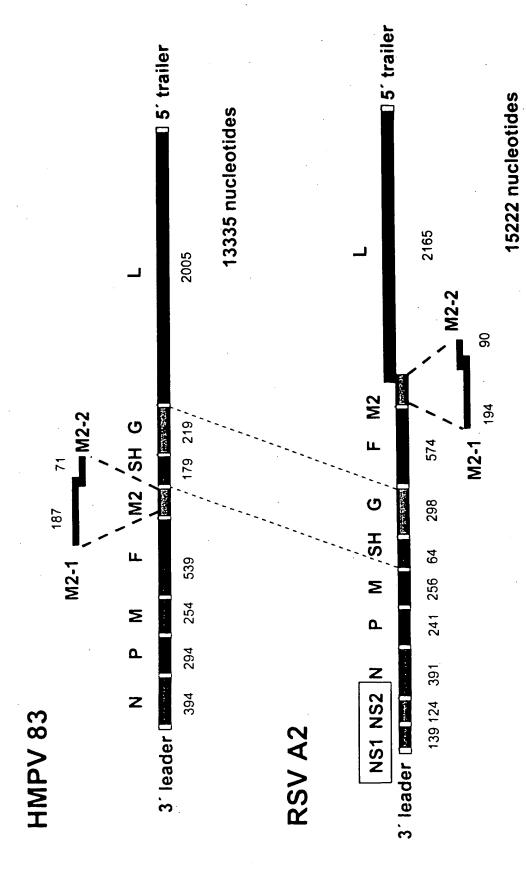
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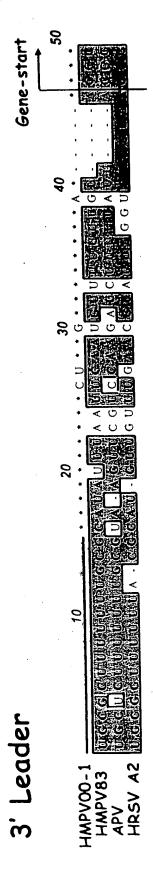
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Attorney Ref. No. 4239-67784
Inventors: Peter L. Collins, Stephane Biacchesi, Urst
Murphy, and Mario H. Skiadopoulos
Title: RECOMBINANT HUMAN METAPNEUMOVIRUS AND ITS USE
Express Mail No. EV331582468US
DRAWINGS: Sheet 2 of 66 Sheets



20

5' Trailer

Sequences previously unknown for any human metapneumovirus

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Examples of differences between HMPV 83 and HMPV 00-1

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190 SIVA SIDS STONHENET GSANING ASVENDANCE ON HENET ASPINSTANT ON	6871 TOCA TOTAL COLOR TOCA TOCATOR A CITATION A COLOR A A GO A A A GO COLOR	83 G nt (cont.) NA TENTRA A MANAGERANA CHEROLOGICA NATIONAL CHEROLOGICA
83 G aa 00-1 G aa	83 6 nt 00-1 6 nt	83 6 00-1

Attorney Ref. No. 4239-67784

Inventors: Peter L. Collins, Stephane Biacchesi, Ursu Murphy, and Mario H. Skiadopou.

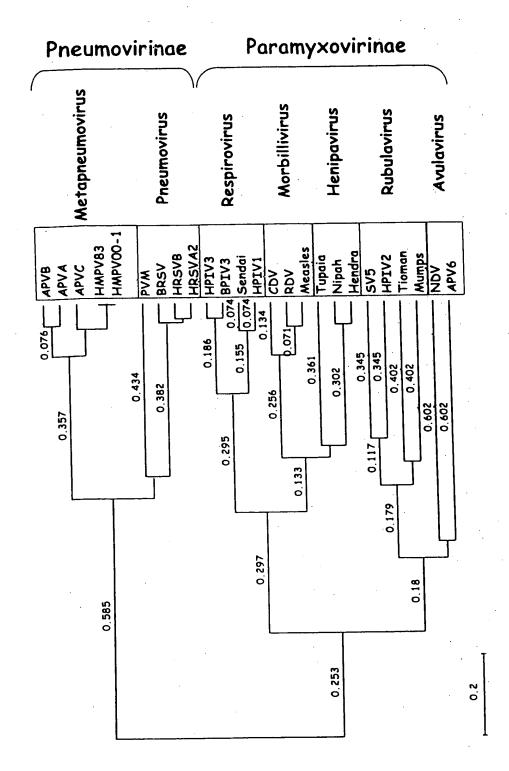
Title: RECOMBINANT HUMAN METAPNEUMOVIRUS AND ITS USE Express Mail No. EV331582468US

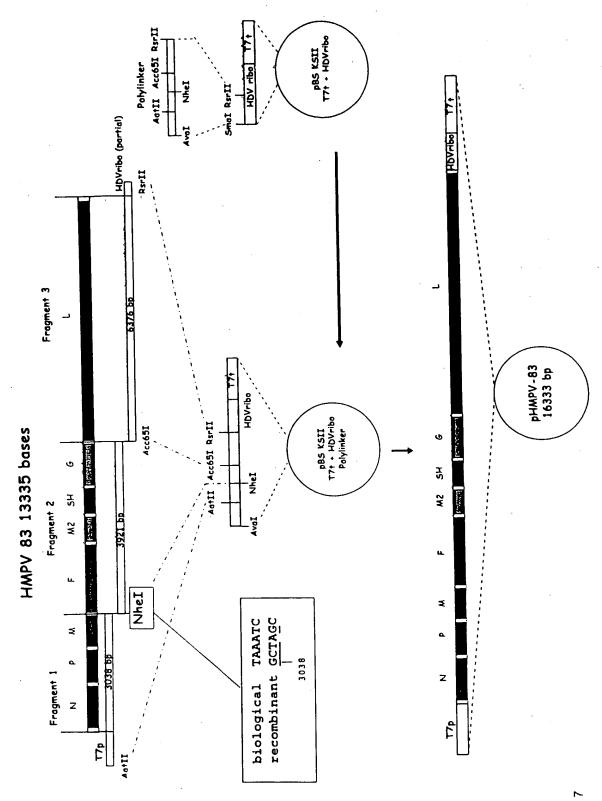
DRAWINGS: Sheet 5 of 66 Sheets

Amino acid identity between HMPV83 and other Pneumoviruses for the indicated proteins

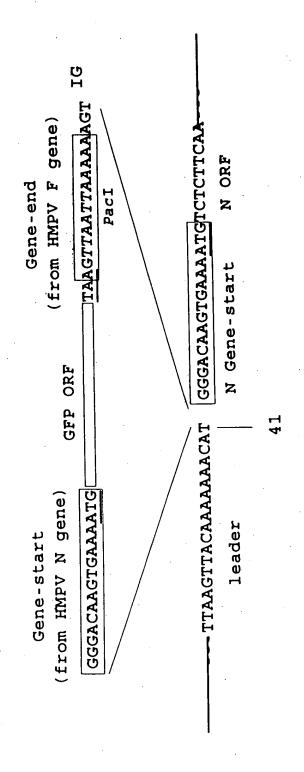
	Z	۵	₹	L	M 2-1	M 2-2	9	SH	L
HMPV 00-1	66	95	66	98	98	96	02	85	66
HMPV 97-82	95	85	76	94	Ž	2	2	2	2
A VA	2	28	11	89	73	25	12	20	64
APV B	69	53	76	67	7.1	27	2	20	Q Z
APV C	88	89	87	81	83	26	2	ΔZ	Ž
HRSV A2	41	31	38	36	36	12	15	9	46
HRSV B	41	31	37	35	35	\omega	12	9	46
BRSV	41	31	37	37	35	14	19	10	46
₩\A	45	28	38	40	36	.12	2	80	2

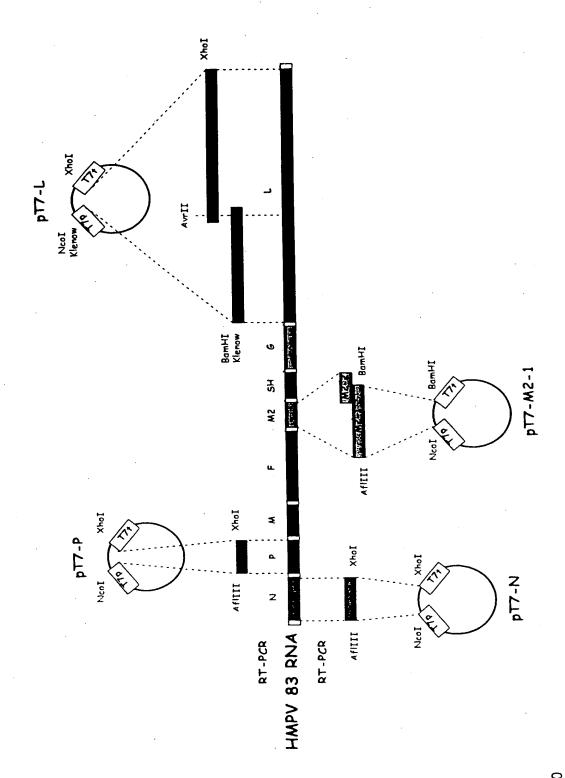
ND: Comparison not done, usually because sequence was unavailable

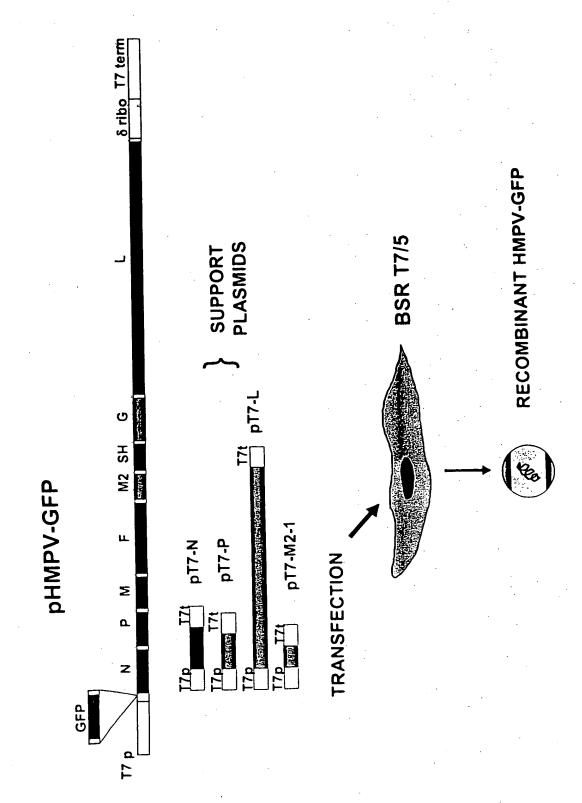


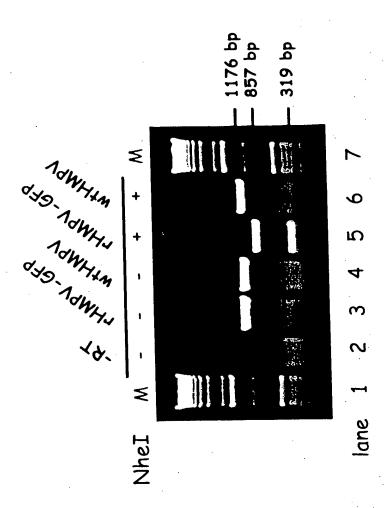


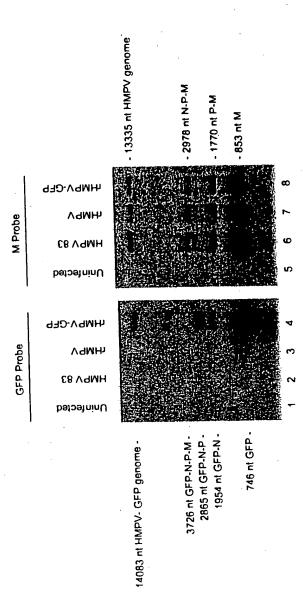
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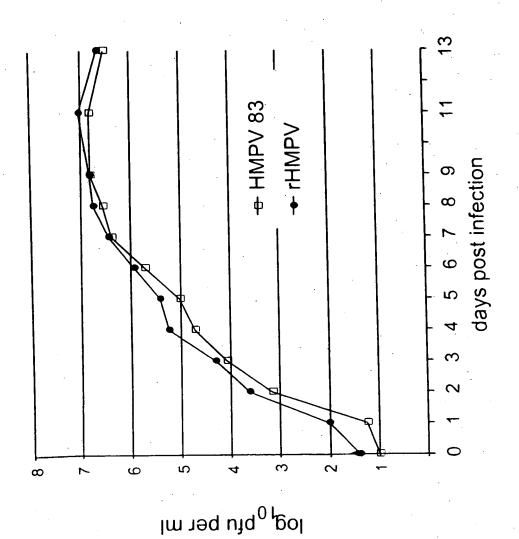
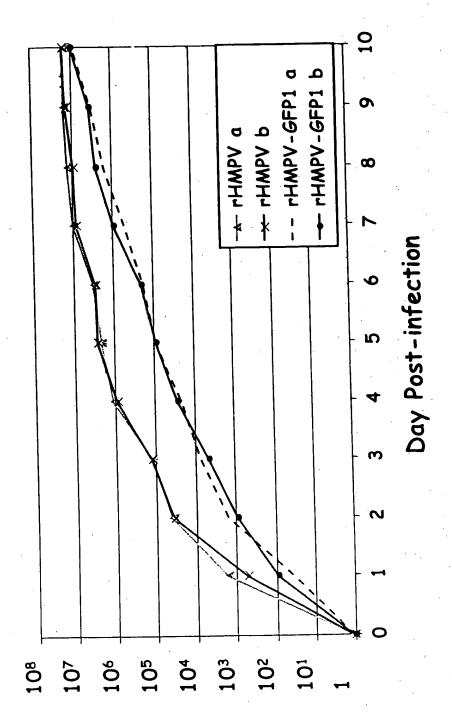
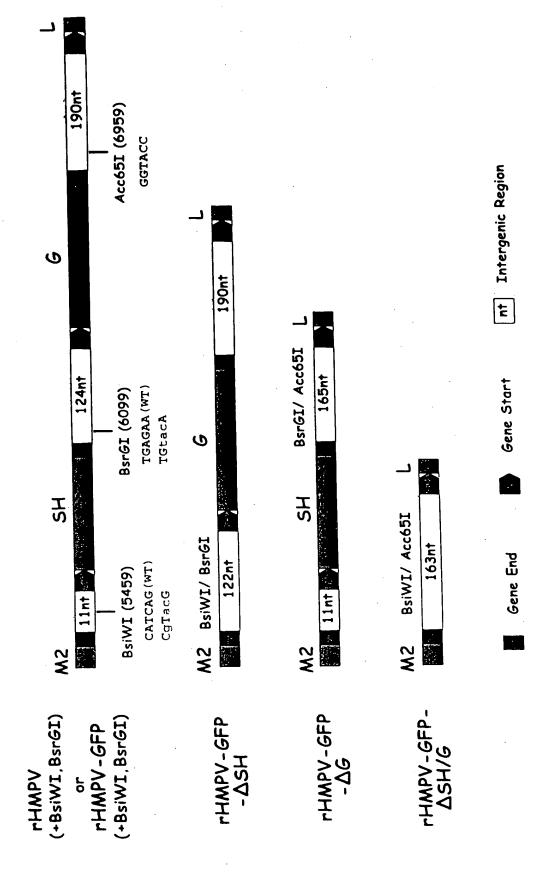
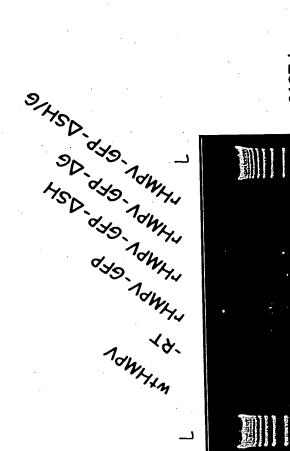


Fig. 13



(Im/utq) natiT suniV





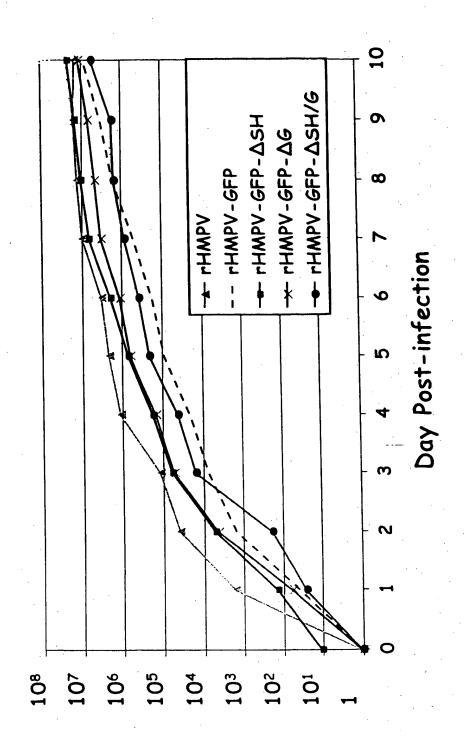
2137 bp 1497 bp 1277 bp 1277 bp 637 bp 637 bp

Attorney Ref. No. 4239-67784

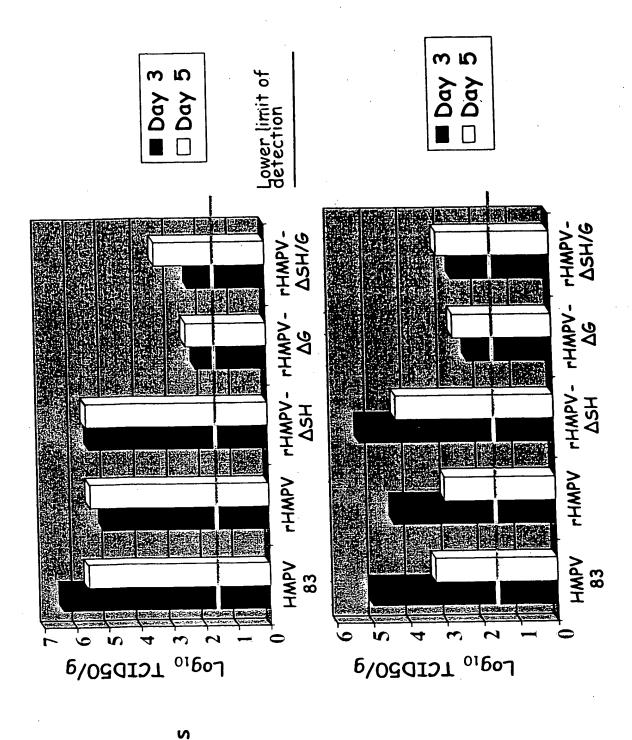
entors: Peter L. Collins, Stephane Biacchesi, Ursula Murphy, and Mario H. Skiadopoulos

Title: RECOMBINANT HUMAN METAPNEUMOVIRUS AND ITS USE Express Mail No. EV331582468US

DRAWINGS: Sheet 18 of 66 Sheets

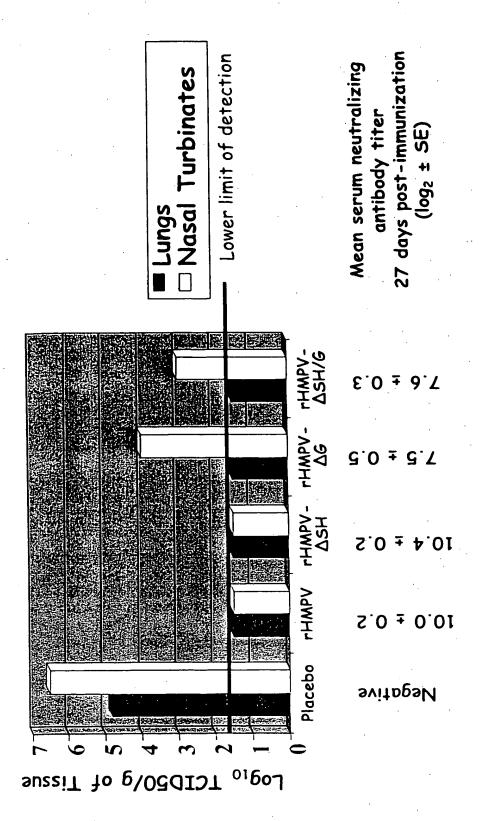


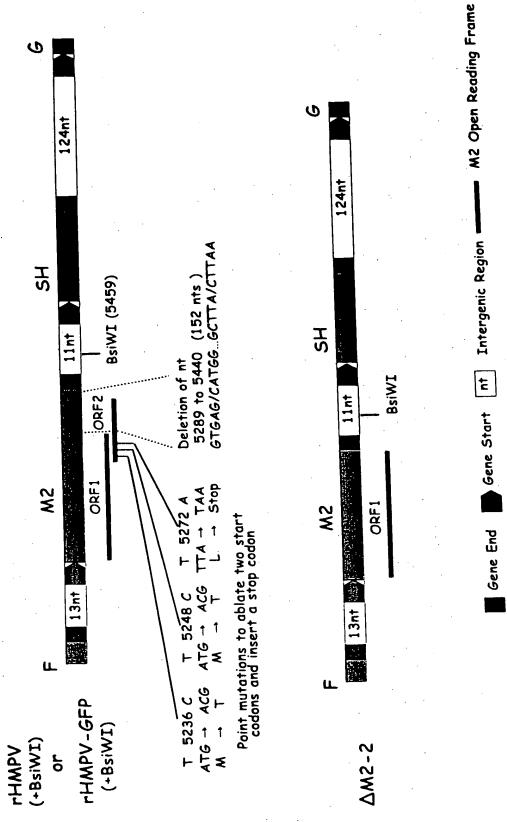
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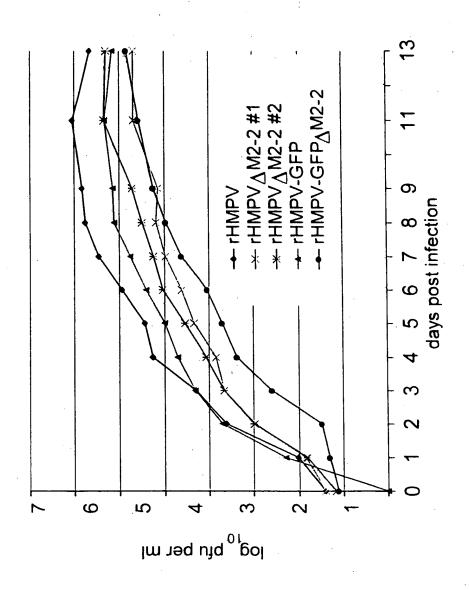


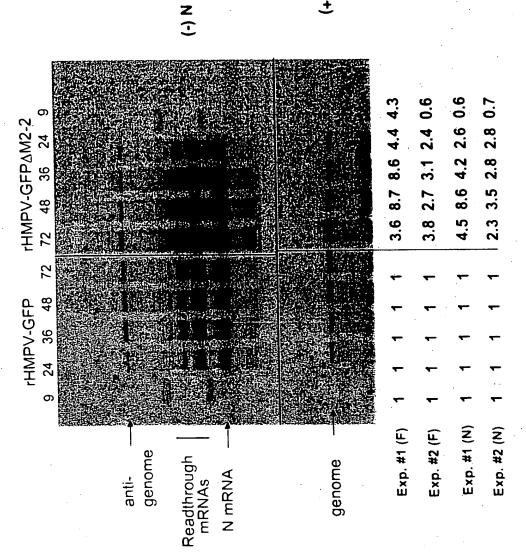
Nasal Turbinates

Lungs



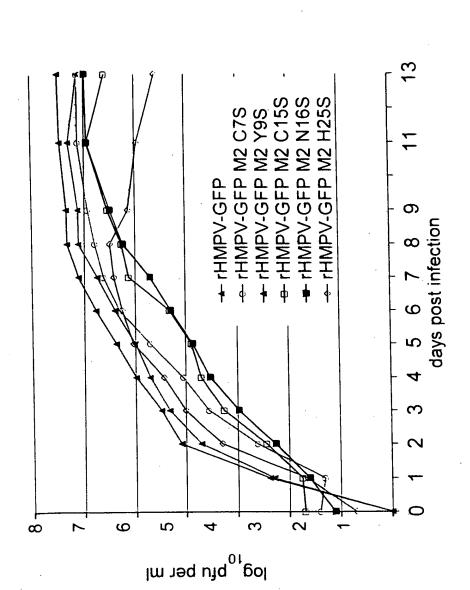






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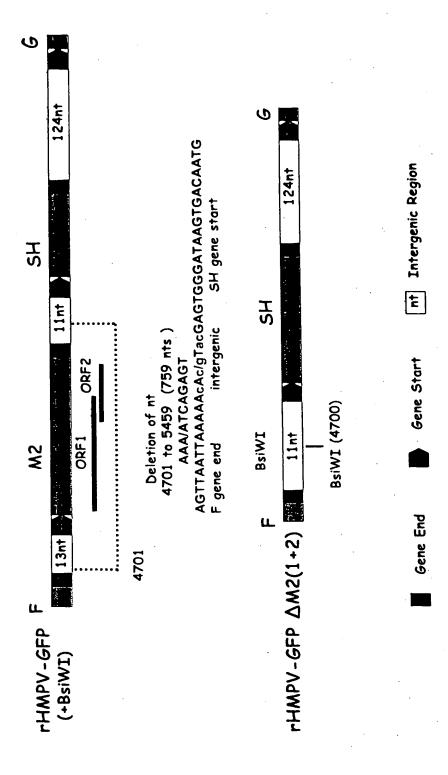
4711 THMPV-GFP ANZ-1

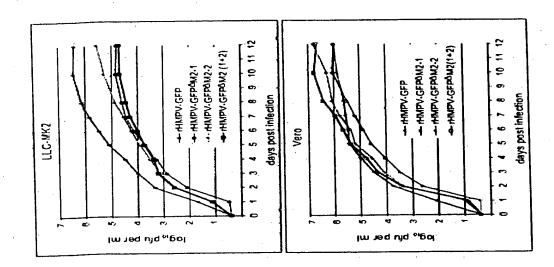
HHPV

HNPV

rHMPV-GFP AM2-1

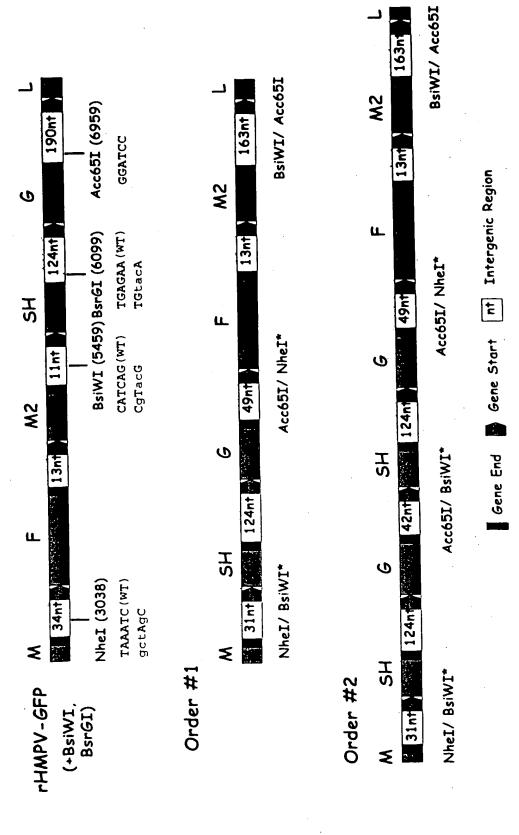
Fig. 21

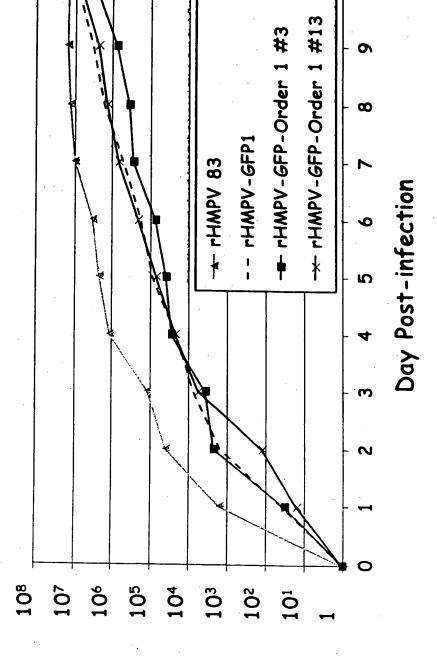




Reduction of virus yield in presence of exogenous interferon (IFN) type I

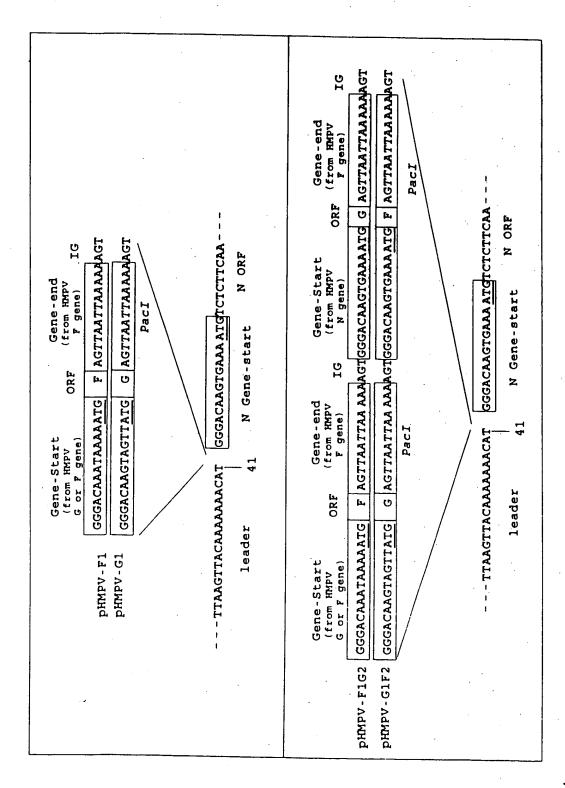
			Fold reduction of virus yield	virus yield
Virus	MO	10 U IFN	10 U IFN 100 U IFN	1000 U IFN
rHMPV-GFP	1.0	5	160	1680
rHMPV-GFP∆M2(1+2) 1.0	2) 1.0	19	1130	no virus
rHMPV-GFPAM2-2	1.0	13	250	no virus
RSV-GFP	0.01	4	17	06

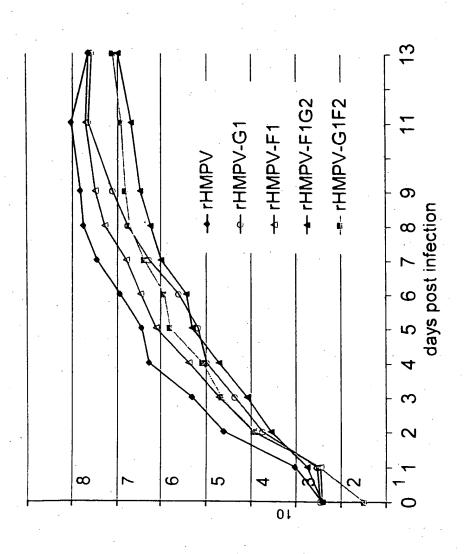




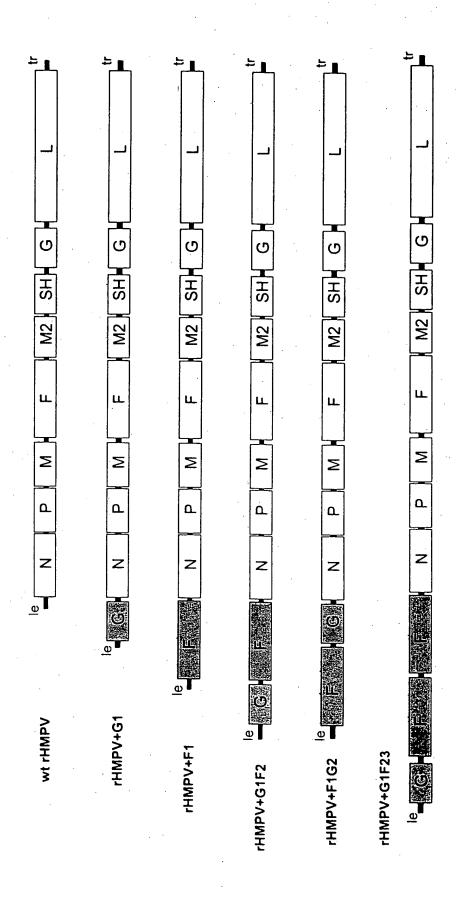
(Im/utq) nstiT zuniV

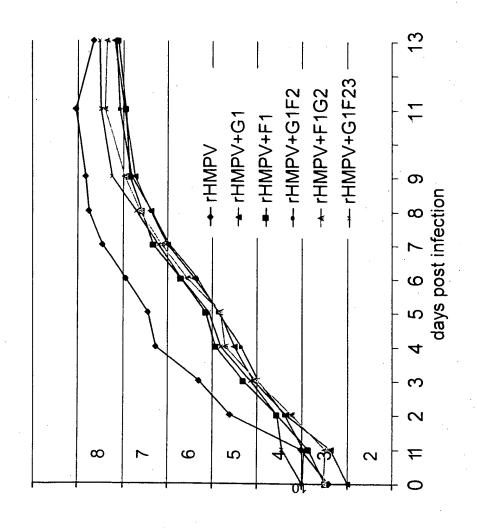
Fig. 23B



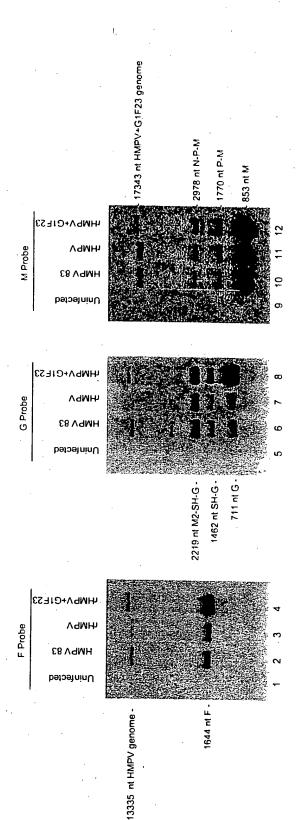


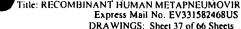
log pfu per ml

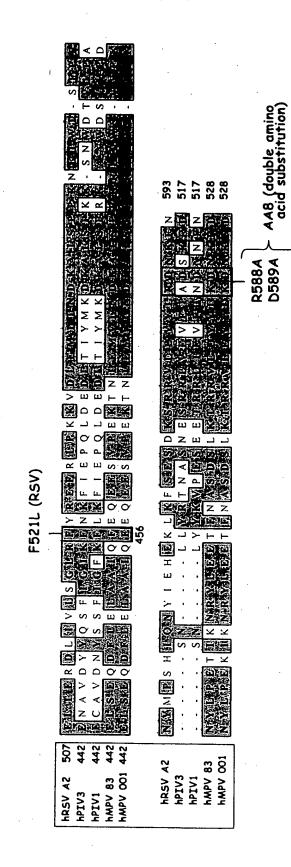




log pfu per ml

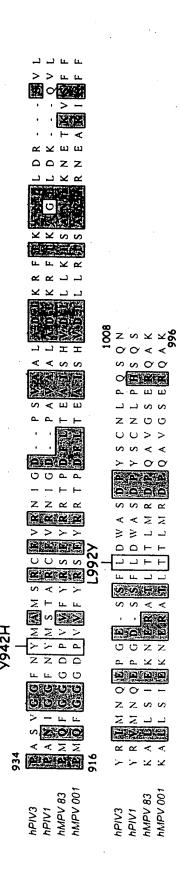






RSV A2 Mutations F521L and AA8





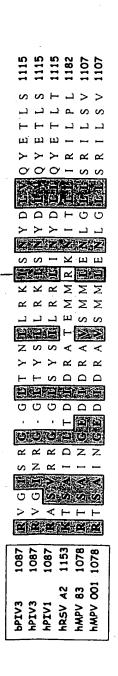
1619 1540 1540

1572 1572

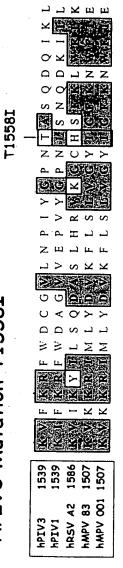
SSZK

BPIV3 Mutation I1103V

I1103V

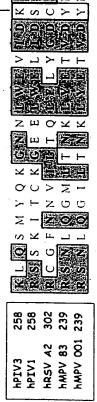


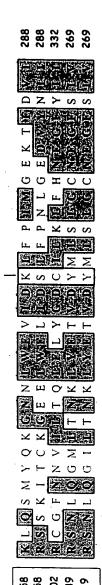
HPIV3 Mutation T1558I



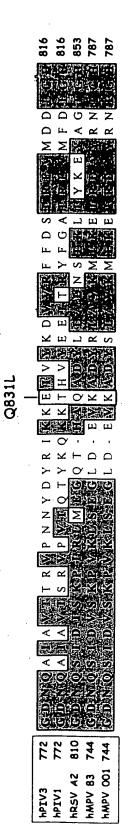
RSV A2 Mutation C319Y

C319Y

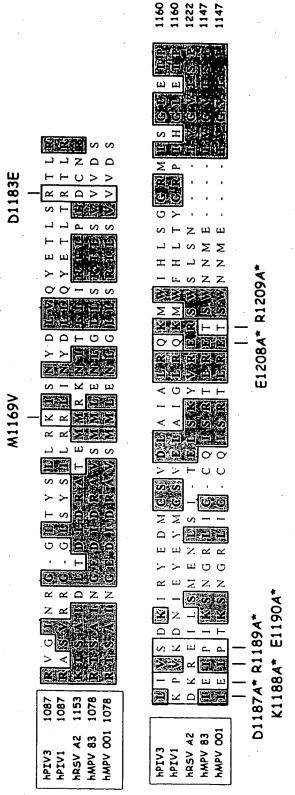




RSV A2 Mutation Q831

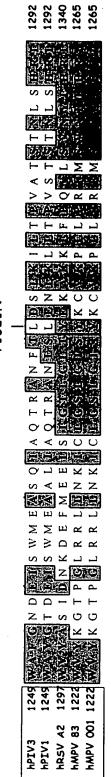


RSV A2 Mutations M1169V, D1183E and C9

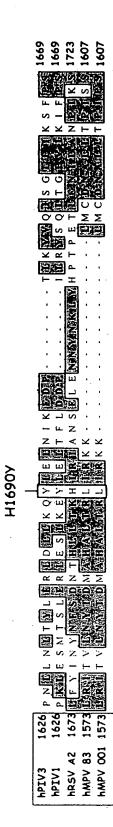


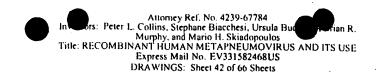
Six point mutations collectively designated C9



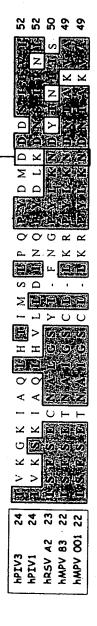


RSV A2 Mutation H1690Y





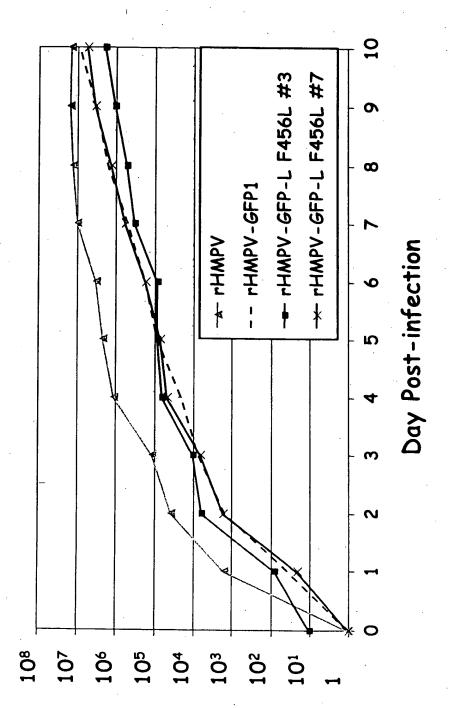
RSV A2 Mutation N43I

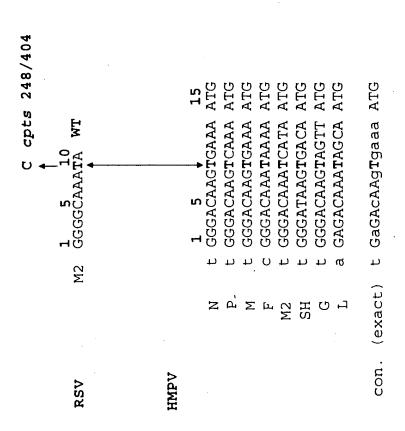


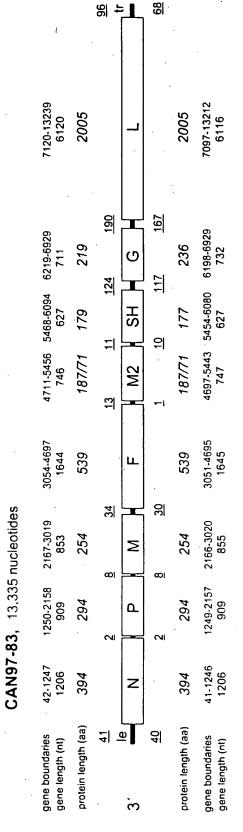
BPIV3 Mutation T1711I

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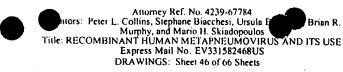
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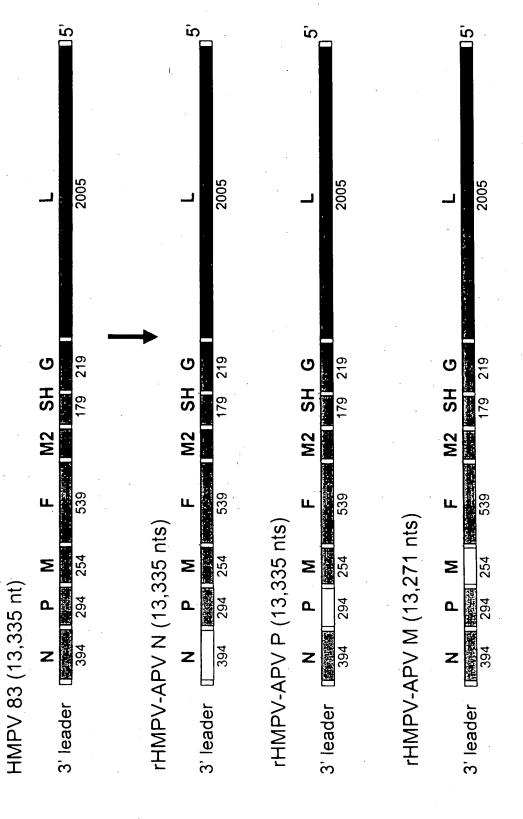




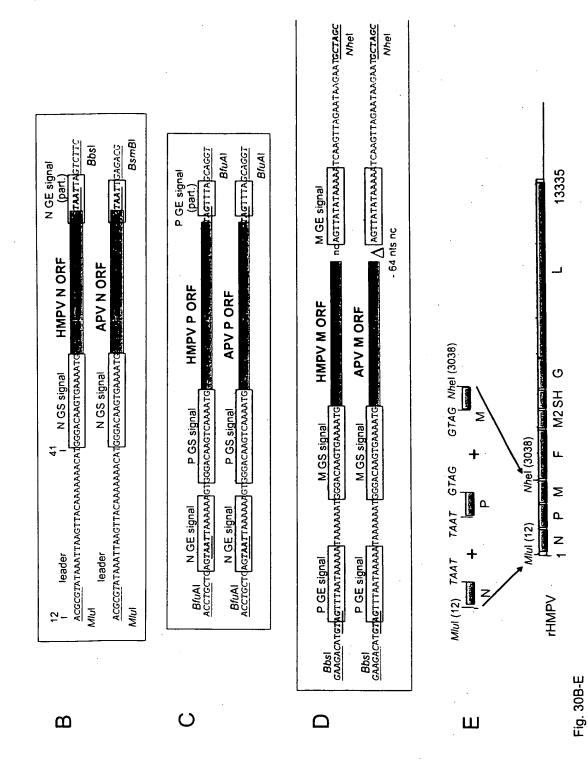


CAN98-75, 13,280 nucleotides





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gene-start	dGGACAAGTGAAATGtetet N (83) GGGACAAaTaAaAATGtetet (75)	GGGACAAgTcAaAATGtcatt P (83) GGGACAAgTcAaAATGtcatt (75)	GGGACAAgTgAaA <u>ATG</u> gagtc M (83) GGGACAAgTcAag <u>ATG</u> gagtc (75)	GGGACAAaTaAaAATGtcttg F (83) GGGACAAgTaAaAATGtcttg (75)	GGGACAAaTcAtA <u>ATG</u> tctcg M2 (83) GGGACAAaTcAtc <u>ATG</u> tctcg (75)	GGGAtAAgTgAcA <u>ATG</u> ataac SH(83) GGGAtAA <u>aTg</u> AcA <u>ATG</u> aaaac (75)	GGGACAAgTagtt <u>ATG</u> gaggt G (83) GGGACAAgTggcc <u>ATG</u> gaagc (75)	<pre>GaGACAAaTagcAATGgatcc L (83) GGGACAAaTaacAATGgatcc (75)</pre>	tr (83) (75)
intergenic		gt ct	taaaaat taaacaat	tcaag- 24 nt-agaac tttag- 20 nt-aaagc	taaaataaaattt t	cacatcagagt taaatagaat	tattt-114 nt-aatat ctcta-107 nt-aaaat	tacga-180 nt-tccaa ctata-157 nt-ttcaa	ttaaa-91 nt ttata-63 nt
gene-end	aatta AGTTA Caa AAAAA Cat aatta AaTT CCaa ACAAAA C-	ttatg AGTaA tta AAAAA ttatg AG<u>TaA</u>ttaAAAAA	tatg <u>tAG</u> TTtaat AAAA catg <u>tAG</u> TTtaat AAAA	atttt AGTTA tat AAAAA attat AGTTA tat AAAAAA	cagt <u>tAG</u> TTAattAAAAA tagt <u>tAG</u> TTAattAAAAAA-	actta AGT<u>TAg</u>taAAAA actta AGT<u>TAg</u>taAAAAA	agttt AGTTA tttt AAAA agtct AGTTA ttt AAAAA	aaatt AGTTA aca AAAAA caagt AGT<u>TAa</u>caAAAAA -	atgat AGTTA att AAAAA ccatt AGTTA att AAAAA
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GGGACAAnTnnnAATG

AGTTAnnnAAAAA

consensus

Percent amino acid or nucleotide sequence identity between the indicated strains of HMPV or RSV

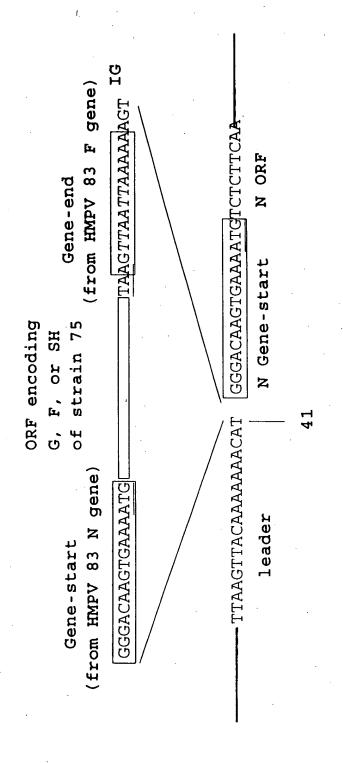
for the indicated prote	leins and ORFs	RS (FS					5		
Viruses	e d	ercent amin	o acid seque	uence iden	tity for indic	percent amino acid sequence identity for indicated protein (percent nucleotide sequence identity for indicated ORF)	C _		
compared	Z	۵	Σ	L	M2-1	M2-2	SH	ပ	
CAN97-83 vs	96	85	97	95	96	88	29	37	94
CAN98-75	(84)	(81)	(82)	(84)	(82)	(87)	(69)	(23)	(84)
CAN97-83 vs	66	95	66	86	98	96	82	70	66
00-1	(94)	(95)	(94)	(94)	(94)	(36)	(88)	(77)	(36)
RSV A2 vs	95	06	91	83	91	61	72	55	92
RSV 81	(82)	(82)	(82)	(81)	(84)	(69)	(77)	(29)	(82)

A. SH protein

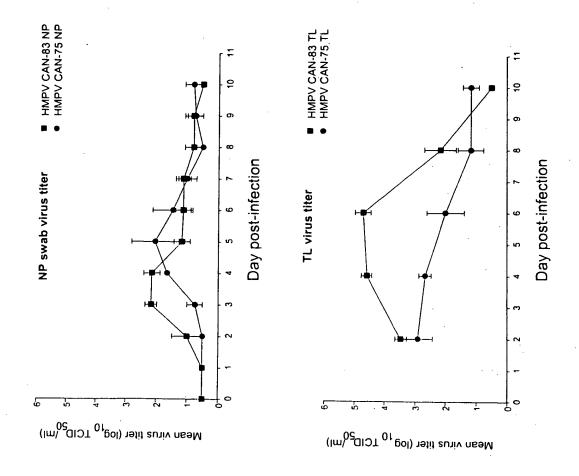
54	54	54		108	107	162	161	161				
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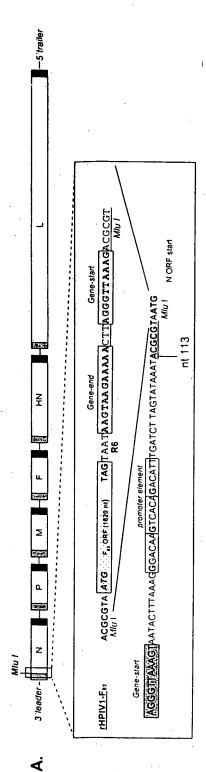
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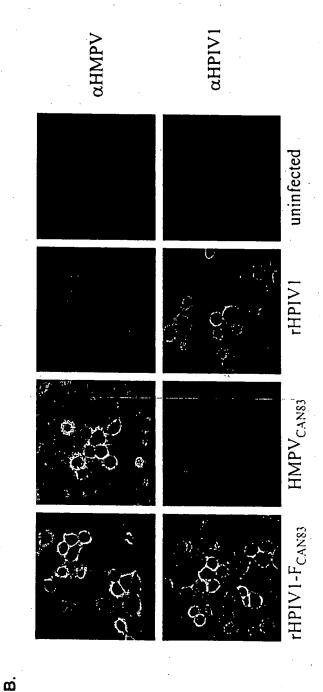
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AR F KM IRS HR T S AP M TL DHA MEVKVENIRAIDMLKARVKNRVARSKCFK NASILILIGITTLSIALNIYLIINYT T ** **** *** *** *** *** *** *** **	TS NMIKV CVNM V PS KTPMT AAD NTK P QA LT DS SLA T 1 IQKTSSESEHHTSSPPTESNKEASTISTDNPDINPNSQHPTQQSTENPTLNPAA 1 M NT S M SR TP VP S T SSP GS YF 1	LEDHLH GTTP A VSQQTT EH TLLRSTNRQ TQ TAEKKPTRATTKKET 1 SVSPSETEPASTPDTTNRLSSVDRSTAQPSESRTKTKPTVHTRNNPSTASSTQS 1 A SP T PPF TH TP A S A K R S R H 1	TT T ST ATQTLNTINQTSNG EA AR RNNA SSDQ TQ ADPS Q 2 PPRATTKAIRRATTFRMSSTGKR-PTTTSVQSDSSTTTQNHEETGSANPQASVS 2 RTA T L T R - S A P I A HKN ASP S T A 2 * * * * * * * * * * * * * * * * * * *	QHTQKSTTTTHNTDTSSPSS- 236 TMQN 219 TRIQRKSVEANTSTTYNQTS 236
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HMPV 83 backbone







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DRAWINGS: Sheet 56 of 66 Sheets

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ATCA	TTTC	AATG	TCAT	GCAT	TCAA	MACC	AATC	TTAA	TATG	GATC	TAGT	CTGT	GAGC	TAAA	GGCA	GATC	TAGA	CTGG	TTTT	ATAG	CAAA	AGTG	TGGG	GATA	GGAT	GAGA	GATA	CCTG	GATT	ATCT	GAGA	CAAA	TTCT	AATA	AAAA		TTCA	LIAI
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HMPV strain 83 (continued)

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13200	AAAATGATGA AGATGACAAA ATAGATGACA ACTTCATACT ATTCTAAATT	ATTC	ATACT	ACTIC	TGACA	ATAGA	GACAAA	AGAT	TGATG	AAAA.	TGCTTGTAAG TAAAAATGA	TAAA	GTAAG		ATACA	ACAGG	AGTA	GATCA	MAACT	13101 TTAAAAACT GATCAAAGTA ACAGGATACA	13101
13100	CACTTACCCT AATATGATTA AACTAATAGA TAACTTAGGG AATGCAGAGA 13100	AATG	TAGGG	TAACT	ATAGA	AACTA	TGATTA	AATA	TACCCI	CACT	TTTTTTGAAG CATTGGAGAA	CATT	TTGAAG	TTTT	ATGAT	AAATT	SAATT	AGGGC	rccaa	13001 AATTCTCCAA AGGGCGAATT AAATTATGAT	13001
13000	GGTTAACAAA CAAAGCAAGT ACAATAATTG ATTGGTTAGA ACATATTTTA	ACAT	TTAGA	ATTGG	AATTG	ACAAT	GCAAGT	CAAA	AACAA	GGTT	CTAAGT	GAGT	ATCATA	CAAG	GGTAG	TTGGC	AACAG	GTAGC)	CTTCT	12901 TCATTCTTCT GTAGCAACAG TTGGCGGTAG CAAGATCATA GAGTCTAAGT	12901
12900	AATAAGAAGG AACTAGATAG ACAGAGAAGA TTATTAACAC TACAAAGCAA 12900	TACA	AACAC	TTATT	GAAGA	ACAGA	AGATAG	3 AACT	AGAAGG	AATA	CCTATA	AATA	SCTAAG	CAGG	TTTGT	TCACT	STAAA	TAATT	SAAGC	12801 CAATTGAAGC TAATTGTAAA TCACTTTTGT CAGGGCTAAG AATACCTATA	12801
12800	AATAGCAGTG TGTAATGATT TTTATGCTGC AAAAAAACTC GACAATAAAT 12800	GACA	AACTC	AAAAA	GCTGC	TTTAT	ATGATT	3 TGTA	GCAGTO	AATA	GATGAA	CTAA	AAAATT	ATAC	GAGAA	CCATG	CCTTG	GTTTA	CAACA	12701 CACCACAACA GITTACCIIG CCAIGGAGAA AIACAAAAII CIAAGAIGAA	12701
12700	AGGGTAGTAA GCTGTCAGGT TCAGAATGCT ACATACTCTT AACACTAGGC 12700	AACA	CTCTT	ACATA	ATGCT	TCAGA	TCAGGT	A GCTG	TAGTA	AGGG	TTATGC	TTCA	SCTACT	AGTT	AGATO	TIGIG	TTTTI	TTACC	TAAAA	12601 CAATGTAAAA TTACCTTTTT TTGTGAGATC AGTTGCTACT TTCATTATGC	12601
12600	ACTIATGGGA CGGACCICTA TITATICGCA AAGTATCAIG CTAAAGACTG 12600	CTAA	TCATG	AAGTA	TCGCA	TITAT	CCTCTA	A CGGA	ATGGG/	ACTT	TGCACT	AATT	ATGCAG	TATC	TGTAT	AAACA	SGAGA	TCTAT	STAAT	12501 AGATGGTAAT TCTATGGAGA AAACATGTAT TATCATGCAG AATTTGCACT	12501
12500	ATTAATAACT TTATGTGATG CAGAATTTAA GGACAGAGAT GATTTTTTT	CATT	GAGAT	CAPCA	TTTAA	CAGAA	GTGATG	r TTAT	ATAACI	ATTA	TGCTTT	AAGA	TAAGCA	AGGG	TACAC	TTTGA	IGGGA	CTCAT	AAAAA	12401 ACTCAAAAA CTCATTGGGA TTTGATACAC AGGGTAAGCA AAGATGCTTT	12401
12400	GCAGAATCAT AGATAGTGGT GAAGGACTTT CAATGGAAAC AACAGACGA 12400	AACA	GAAAC	CAATG	ACTTT	GAAGG	AGTGGT	r AGAT	AATCAT	GCAG	CCTTGATCAT CATTATCCTC TGGAATACCA GAGAGTGATA GGTGAATTAA	GGTG	STGATA	GAGAC	TACCA	TGGAA	ICCIC	CATTA:	ATCAT	CCTTG	12301
12300	GCATGTGAAT ATCCTGATAT TAAATTTGTA TATAGAAGTC TGAAAGATGA 12300	TGAA	AAGTC	TATAG	TTGTA	TAAAT	TGATAT	r ATCC	GTGAA	GCAT	AGAACA	3255	LTGGAT	GAAA	AGCAG	GAAGG	rrgga	CTTTA	ITGTA	12201 AAGTITIGIA CITIATIGGA GAAGGAGCAG GAAATIGGAI GGCCAGAACA	12201
12200	AGTIAGICIG AAAACAIGIA IIGGAAAACI TAIGAAAGAC CIAAAICCIA 12200	CTAA	AAGAC	TATGA	AAACT	TTGGA	CATGTA	3 AAAA	AGTCTC	AGTT	TTTAGTTCTA CTGGATGTAA	CTGG	STTCTA	TTTAC	TIGIC	TAACT	AGATA	TTAAT	SCATG	12101 TGGCAGCATG TTAATAGATA TAACTTTGTC	12101
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	100	GTGCCCATCC	GAAGCAGCAC	GTGAAGTTCG	ACAACAGCCA	CGCCGACCAC	AACGAGAAGC	GGACAAGTGA	GCACAACAAC	AGAAATAGGA	ACGIACICCI	AAGCAAGAAA	TGTAGGTGCC	AGATACCCTA	CATTAGGCTC	CATTGCCAGG	CCTGAATCTG	CAGGCTTAGG	AATTAACTTT	AAAAAGTGGG	AAGAAAACCT	CCGACCATAT	AAGAAGAGTT	ATTTACACCA	ACCTTCGAAG	ACATTGCTAC	GGGAAAAGCA	ATTGTTGAAG	TGTAGTTTAA	CTAGTAGAAA	TGACTATAAC	TGAAGTCAAT	CCATATGGGA	ACACACCAGT	TCTAACACAA	GTTATAGTAG	AACAGCCAAG	CAATCAAGAA	
		GTGC	GAAG	GTGA	ACAA(ညညည	AACG/	GGAC	GCAC	AGAA	ACGT/	•	TGTAC	AGAT/	CATTA	CATTC	CCTG/	CAGG	AATT!	AAAA	AAGA	CCGAC	AAGA	ATTTA	ACCTT	ACATI	GGGA	ATTGI	TGTAC	CTAGI	TGACT	TGAAC	CCATA	ACACA	TCTA	GTTAT	AACAG	CAATO	
	90	CACCGGGGTG	CCGACCACAT	CCGCGCCGAG	GAGTACAACT	GCGTGCAGCT	CAAAGACCCC	TAAAAAAGTG	AGAGATGTAG	AATATGCTGC	TTAACCAGA	ATAGACAAAG	TCTTATTATG	TGCACTCAAA	TATGGCAAAG	SGTGGGGAGT	AGAAATGGGC	GGCAATGCCT	AAAGCAATAA	TGAGTAATTA	AAAAATCATT	ACCTACCAAA	CCTATTGAAG	AGAAGGTCTC	CTCAATCTTA	AGAACACTCA	AAGAAGCCAA	GCTCAACAAA	CAGTTAATTA	ICAAGTTGAT	CTAAAGACTC	CCAAAAAGTT	AACCATGAAA	CTAGAAAAGA	CAGACCAAGC	FGGGACCCAA	AAGTCCAGAT	AGAATGCTAG	
	_			CCGCC	_	_	_	-	-	-	TITA	-	TCTT	TGCAC	•	GGTG	•	GGCA	AAAGC	TGAGI	AAAAA	ACCTA	CCTAT	AGAAG	CTCAA	AGAAC	AAGAA	GCTCA	CAGTT	TCAAG	CTAAA	CCAAA	AACCA	CTAGA	CAGAC	TGGGA	AAGTC	AGAAT	
	80	AGGAGCTGTT	AGCCGCTACC	ACTACAAGAC	GCACAAGCTG	GAGGACGGCA	CCGCCCTGAG	GTAAGTTAAT	TACAATAAAG	GCTGATTACA	TCCAAGTGGT	GGTGGAAGAG	ACACCTATAA	TACTAAGTGA	GITCAITGAG	ACAATGCTGA	ACCTGGTGCG	TGTTGTTCTC	AGTTTGAAAG	AAAATGATTA	GAAGCTTTCC	CTATCAGTAG	AGTTATGGAT	AATACTAAAA	ATGCAGAATC	AGGGCTATTA	GACATAATAA	AGGCAAAGGA	TGACATTTAC	CAGCAGCTGT	GCTTGATCAG	TCTGTACTTC	TTTACTTAAC	TTTTATGGAT	AGCAGTGAAG	AGCTTGGAGC	ATATGTGCTG	AGTTAGAATA	
			-			-	_	_		GCTG	•		-	-	GTTC	-		-		-	-	CTATO	AGTTA	AATAC	ATGCA	AGGGC	GACAT	AGGCA	TGACA	CAGCA	GCTTG	TCTGT	TTTAC	TTTTA	AGCAG	AGCTT	ATATG	AGTTA	
	07	AGCAAGGGCG	SCAGTGCTTC	GACGACGGCA	ACATCCTGGG	CCACAACATC	AGCACCCAGT	AGCTGTACAA	AGTCTCAGTA	TGCTAAGCAT	GGCAGTGAAG	AGAAAAGCTG	AGCACCAGAC	GCTAACCGTG	ACAGAAGTTT	TGCTGGTCAA	SAAGTCTATG	ACTITGCAAG	CTATGCCAAG	SACGACAGTC	AAAATTGGCA	GAATTACCTA	AAACAATCAA	ACCATCAACC	GAAGAAGAAG	GCATGATATT	ACTAATAGCA	TTAACTGAAA	ATCAAGAAGA	ATCCCTTACA	CAGCAGTTCT	TGCAGCAATG	GTAAAAACAG	CATTATGCGA	AGCTGCAATA	ATATTCAAGA	AAGGAACAAG	ATAAAAATCA	
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	09	GAAAATGGTG	CCTACGGCGT	CTTCTTCAAG	GAGGACGGCA	TCAAGATCCG	CCACTACCTG	GGCATGGACG	ATATTAAAAG	AAATTCTATA	AAGAAACTCA	CACGGAGTAG	AGAGGCCTTC	AGTCAGAAGA	AAAGTGTATT	AAGCTTACGG	ACAAGTCACA	AATTGTCCCA	CAGCAGAAAG	AAATGTGAGT	ATGAAGCGGC	TGAAACATTG	GAAGCAAAGC	AGAAGTTGAA	TTCAGACAAT	GAGAAATTAA	TAAGGGAGGA	TAGTGTAAAA	CAGGAAAATA	CTATCAAGGC	AATACACCAC	CGGCCCAGGG	AGTCTGTGAA	SATCTAATCG	CCACTGTTGA	TCCCAAAGGC	TGGAGCCATC	rttagttat	
		GAAA	CCTA	CTTC	GAGG	TCAA	CCAC	GGCA	ATAT	AAAT	AAGA	CACG	AGAG	AGTC	AAAG	AAGC	ACAA	AATT	CAGC	AAAT	ATGA	TGAA	GAAG	AGAA	TTCA	GAGA	TAAG	TAGT	CAGG	CTAT	AATA	Ü U U U U	AGTC	GATC	CCAC	TCCC	TGGA	TTTT	
	1 50	TGGGACAAGT	ACCACCCTGA	AGCGCACCAT	CGACTTCAAG	AAGGTGAACT	TGCCCGACAA	GATCACTCTC	CAAGCATGCT	LTGTGTGGAG	AGCAGATICT	GTTAGACATA	CCACAAAATC	TAGAGACCAC	ATTTGAACAA	ATATTCATGC	CTGAGTTAAA	ATCACTAGCC	CTATTTTCAG	AACACTTTCT	LTCATGGGTA	ACACTGTATC	AATCAAAACT	CCTGCAGAAA	TAGACTTGCT	ATCGATTGAG	ATGATTGGCA	TAGGAAACGG	AAAAGACACA	TGGTAGACAC	GTTTCAGGCC	GTGAATGCAT	ACAAACTTAC	AAAAACACAT	AGTGAATCAG	CCATGAACAA	ATGCAAGACT	AAAGTCGCCA	
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	40	CAAAAAAACA	CACCCTCGTG	FACGTCCAGG	TGAAGGGCAT	GAACGGCATC	CCCGTGCTGC	ອອລລອລລອລລ	ATCTATCATA	AATAACACTA	GAGAGAGTAC	ATTTACAGAT	AGGCAATATI	GAAGTGGGAT	ICTATGATTT	ATTCGTTAAT	ICTGICCAAG	CTGGACTGTT	AAACACAGAA	GAGGCTGCAG	AGATATTCTT	GAAAAAGTGA	AAGGTGGGGC	TGGGAAAACT	AAAGATGCTC	CCAGACTAGA	CAGAGATGCA	CGGACAAAAA	AAGAAGAACT	GAGTCCTATC	GGTTCCCCCT	AATACTAAAA	TTAGAATTTG	CAGTTGGCAA	TATCAAGGAG	ATGATTATGA	TAAGTAAAAT	TATAGACTAA	
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	j 30	PAGGTTA	TGCCCTGGCC	GCCCGAAGGC	TCGAGC	GCAGAA	GACGCC	TCGTGA	CACCTGAGTG	TGCAACAAGA	GGATCA	GAGAAG	ATCATC	ATCAACTATA	GATCTT	AAGTTT	AGGACATGTA	AGCCCAAAAG	GGAGAGTGCC	TGAAGAAAAA	AGGAAA	ATAGGA	CAGACA	CAGTGA	TTGGAG	TTGAAG	TGGGAT	AACCAG	AAGAAG	AAAATG	CTAACAATAT	TGGTCC	AGCAAA	CCAAAC	AGTTTC	CTGATC	AAAGCA	CTATTC	
	0	AATTAA			-						C TCTAGG	C AAAGGA	A AAGAAT		C GCTAGA	3 CAGAAA					CTGAAG	TATTAT	A TGGACA	CCTCCA	: AAAGTT	A AGCATT	A GAGATG		A TCCGAA	AGTGAA		: AAAGTG	ATATAG	TCGGCC	A AATCAG			AACTCT	
	20	AACGCGTATA	AAGCTGCCCG	AGTCCGCCAT	CCTGGTGAAC	ATCATGGCCG	ACACCCCCAT	GGTCCTGCTG	TCAAGGGATT	CCCTCATCAT	TTAGCACAGC	TAAAAACAAC	ACTITGCTTA	CCAAACTAGC	ACCAAAAATC	GGCAGCAAAG	ATATAATGTT	TTTAAGGCAA	ATGTATCGCG	GACTCACAGA	ATGTCATTCC	GATCTCAATC	GAAGTTAGCA	AGGGTGCTGC	GAAAATACAC	TTCATCATTA	ACAGCAGCAA	TGGAAGAAGA	AAGTGGTGAA	AAATGGGACA	ACCTGCAAGC	GCTGCATCAC	CACTTGACGA	GTTTGTGAGC	GCATTTATCA	CACCTTATGC	ATATGTCCAG	AAGAACTACC	
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;	rhmpv-GFP 1	ACGCGAAAAA	CACCACCGGC	GACTTCTTCA	AGGGCGACAC	CAACGTCTAT	TACCAGCAGA	GCGATCACAT	AAATGTCTCT	AGCAGTGACA	ATACAATATA	TGGGGAAAGT	AACAATGGCA	TTAATATTTA	GGATGGACAT	ATCCTCTACA	TCATCTAACA	GGCTCCTACA	CATAATAGGT	TCTTCATTAG	ACAAGTCAAA	AGTCATAAAA	TGTCAGAGCC	TACTGAGAAA	AATGAACCAG	AAAGAGATAC	AGCAGGACCC	GCAGAAATGA	ACGAGAGCAC	TAAAAATAAA	AGGACCTGTT	TACTCTGTAT	GCGACTGTAG	TGGTATCAAA	TACAATACCA	GCCAAAATTG	AACTAGGAGC	CAACCTGACC	
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AATCATGTAG GAACAAATTG GAACCATCCG AACTGCAGTG TTCAGTCAAT AACTAGCCAG GATAGGGGTC	STGAAACAAG CCCATGCAAA SGCAGCAACA AGCTAAGCAA	ATAA STGG ATGA ATTA ACCA ACCA	SCCC VAAG VAAA VACA VACA VACA VACA VACA V	TCA AAA AAA
AATCATGTAG GAACAAATTG AAACCATCG AACTGCAGTG TTCAGTCAAT TACAGTCAATGAATG	GTGAAACAAG CCCATGCAAA GGCAGCAACA AGCTAAGCAA	ATTGTAATAA AGCTGAGTGG GCAAATATGA CTATCTATTA GGTTCCACCA AAGTTGAAGT	TCATATGCCC GAATTAAAAG ATAATTAAAA GTAGAAAACA GCTGAAGCAT TATAACAACA AATTAACAGC AGTAGAGAACA AATTAACAGC AGAACCCGCA	TCCGCAGAGC AACAGGTTCA FAAAGTAAAA CTGGGAGAAA
AAA AAA AAC AAC AAC	610 660 860 860 860 860	ATT AGC GCA CTA AGG	TCA GAA TAA AAT AAT AAT AATA AAA	TAAC
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TACCTAGAGG AAAACCTTAC SGCAAGAGGG SCAATTGCCA SAGTGTTGGC ACAGATTGCCA TCGGAATCCTTGCCA TCGGAATCCTTGCCA	SAGAAAGACT CTACAAATTA CTGTTCCATT ACTGTATATC TCAATGTTGC	TGGCTTCATC GCACCTCCAG AAGGCTCCAT TAAGATCAAA TTTTGTTCTA CAACTACAAG	CAATGACTCT GACTCAAAAA ACCTCAAAAA TTACATAAAA AATGCACAAA AATGTTAAAAC AATAGGTAAT TGGAGGTGAA TCGCCCCAA	ACGAAGGCAA ATCATGAAGA GAGATAGCTC TCAAATCTCT
TAO AAA GGG GGG GGG GGG TCG	SAC CTA PCT PCT PCT PCT PCT PCT PCT PCT PCT PCT	GCA CAA CAA	CAA GAC AAG AAT AAT TGG TCA	ACG ATC GAG TCA
SAGC STAG VATT STTC SAAT VAAT SAGC	AAAT AAG	TAC GGG TAAA AGA TGA	TGA AAA AAC ATC ATC ATC AAT AAA	ACA AAA TAC TGC
TAAAGAGAGC GGTGATGTAG CTGACCAATT AGCAGGTGTT AATGGAGTTC ACCTAAAAAT AGAAAGGGGT	CTACCCAAAT AACATATCCA AAGGAGTAAG AATAGACAAC	AAGGGAATAC ACCAACGGA AATGTCTCGC TACTTATTAA GAACGCAAGA CATAATCAAG	CAGGCGCTGA AAATGATATG AAATGATATG ACATGTACAA AGCCAGAAATC CCAATCTTGA ACTTCATAAA CTTCATTAAA CTTCATTAAA	ACGGCAACA ACAACCCAAA CAAAAAATAC TCAGCTTTGC
		AAG AAT TAG GAA CAT	CAG AAA AAC AAC GAA CCAA ACC ACC ACC ACC	ACA CAA TCA
AACACGGTCT ATTAGAGGTG ACAGTCTCTG CTGCAGTCAC TACATTGGGG GACATTGATG CAATATCTTT GATGGTGCGA	CAACTGTTTA GTGCAACATC GCTTGCTACA ACACAGTGAC	AGTGCAGAGA AAACAAAGAA SACAAATCAT SCCAGATAGA GGGAAGACA STCTACACAA	FCAG SATG SATG SATG SAAA SACA SGGA SGGA SGGA SGGA SGGA SGG	ACC TAA TAA
AACACGGTCT ATTAGAGGTG ACAGTCTCTG CTGCAGTCAC TACATTGGGG GACATTGATG CAATATCTTT GATGGTGCGA	CAACTGTTTA GTGCAACATC GCTTGCTACA ACACAGTGAC	AGTGCAGAGA AAACAAAGAA GACAAATCAT GCCAGATAGA AGAGAAGACA GTCTACACAA	GACTIATCAG GAGGTTGATG ACATAGAAT GTCTTCAAAA ACAGTAACAA CTGGAAATA GATCTATGCA AAATATGGGA AAATAGGGA AAATAGGGAACAA	AATCCCCACC CAGCAGCACC AATTAGTTAA CGACACCATG
				AAT CAG AAT CGA
ATAACACCTC ACGITITIAC ACGITITIAC ACGICAAA SCAACAGCAG AAGCAGTATC AAACAAGTGC ATAACACCGGG AGAACCGTGC	AATGCAGGGA AATCAAAGGA GGCTCTGGTT CAAGATGCAG	AATCCTAAGC ATAATCAAGA TAAAATTTGG ACTGGAGGTTG AGGCGCAGGC	GCTGATAATT CATTACTATA AAAGTGATGA AACATTTTC AACAATTTTC AACACTCAA CACACTCAA AATAGGTAAC AATAGGTAAC AATAGCATAAC AATAGCATACAA AATAGCATCAA CACACACAA	ACCA CCGA CCGA CCGA
ATAACACCTI AGGTTTTTAA AGGACTCAA SCAACAGCA AAGCAGTAT AAACAGTG ATAACACCA AGAACCGTG	AATGCAGGG AATCAAAGG GGCTCTGGT CAAGATGCAC TTGATCCAAT	AATCCTAAGG ATAATCAAGA TAAAATTTGG ACTGGAGTTG AGGCGCAGGG	GCTGATAATT CATTACTATA AAATTTAGAAA AAAGTGATGC AACATTTTC AACACTCCA TAGACTCAA CACACTCAA CACACTCAA CACACTCAA CACACTCAA CACACTCAA CACACACA	TCCAGTACAC TCCAGTCCGA TATAAAACCA
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FFGAAOOFF			A ATTAGCAAA A GTCCTGTTTT A GATGTCATTA A AGACTCACCA A ACAGTTGTGA A ATTTGAG A ATTTGAG A ATTTAGAA A ATTCAAAAA A ATTCCAAAAA	
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AATTAĞCATA ATGAGTGTAG GTGTTTCAAG GGAAATTCAA	CACTATAAAA	CATTGGTGTG	AAATATTCCT	ATTGTTAAGG	TCACTAGTAG	TGGTTGAGAT	CACACGATTA	CAATTAGATT	TATTGCCATG	AAATCCTAAA	AAAGATGACC	CAGACGCAAC	TTTTTTAAG	AAAGACTGCA	CACTAGGCCA	CAATAAATCA	CAAAGCAATC	ATATTTAAA	TGCAGAGATI	TCTAAATTAA	AAAATAAGAA	50
A ATG																						40
AATTAGCATA GTGTTTCAAG	TGCTCATGCC	ATTAGCATGT	ATGGACTTCA	CAATAGATAA	AAAATTCCTA	GAAGGTGATT	CACATGCTCT	TCCCACAACA	TACATGATAC	TGAAAGACCT	TAGAAGTCTG	ATGGAAACAA	ACAGAGATGA	GTATCATGCT	ATACTCTTAA	AAAAACTCGA	ATTAACACTA	TGGTTAGAAC	ACTTAGGGAA	TTCATACTAT	AAGTTTATTA	_
G AAT									T TAC	A TGA												30
SCTGTG	SGGAAA	TATCAGCAGC	TCATGCTTTT	SATGA	TATATGATGT	TGTCAATGCC	ACAGATATGG	ITATT	AAGAAA	AAACTT	FTGTATA	ACTITO	LTTAAG	TATTCGCAAA	ATGCTA	TATGCTGCAA	SAAGAT	ATTGAT	ATAGAT	IGACAA	LATCAT	т —
A TCAC	A CTAC	r TATC	A TCA1	A GTAC	r TAT	r rgr	I ACAC	C AAG	r AAC	r GGA	A AATT	A AGG	A GAA7	r TAT	AGA	r TATC	2 AGAG	AATA	A CTAP	r AGAT	A ACCT	
11801 CTTGGTCTTC CAAAATGCAA TCAGCTGTGG 11901 TTAGAAGAAA TAGACATTAT GCCACCACCA	ACAAAATAGA TATGTTAACA CTAGGGAAAA	AAACAATCTT ATTGAGTCTT	GGTGACGGGT TTATATCAGA	ACATTAAAGA TGAAGATATA GTAGATGAAT	12401 GGTTAAGAAA AGGATAATGT	TTGCATGAAA TACCTTGGAT	GAATAACTGT TTTGAACTAT	CCCAATGGTT AACTTAACTC AAGTTATTGA	AATTATGCTA AAGGGAAGCT AACAAGAAAT	TTAGTCTGAA AACATGTATT GGAAAACTTA	13001 ATGTGAATAT CCTGATATTA AATTTGT	13101 AGAATCATAG ATAGTGGTGA AGGACTTTCA	13201 TAATAACTTT ATGTGATGCA GAATTTAAGG	TTATGGGACG GACCTCTATT	GGTAGTAAGC TGTCAGGTTC AGAATGCTAC	TAGCAGIGIG TAATGATITI	TAAGAAGGAA CTAGATAGAC AGAGAAGATT	TTAACAAACA AAGCAAGTAC AATAATT	CTTACCCTAA TATGATTAAA CTAATAGATA	13901 AATGATGAAG ATGACAAAT AGATGACAAC	14001 ATCAAAAGTT AAAATTTAAA ACCTATCATT	20
CAA!	A TATO	r ATT	r TTA	A TGA	A AGG	A TAC	r TTT	L AAC	A AAGC	A AAC	CCTC	3 ATAC	[ATG]	GACC	TGI	TAA1	A CTAC	AAGC	A TATC	S ATG	AAA	_
GTCTTC	VAATAGI	AATCT	SACGGG	LTAAAG!	FAAGAA	CATGAA	PACTG	VATGGTT	ATGCT	TCTGA	GAATA	TCATAC	PACTT	GGGACC	GTAAGO	AGTGTC	AAGGA	CAAACA	CCCTA	ATGAAG	AAAGTI	10
1 CTTG			1 GGTC	1 ACA1	1 GGT1	1 TTGC			l AATT	1 TTAC	1, ATG1	1 AGAA	1 TAA1	L TTA1	1 GGTA	1 TAGC		-		1 AATG	1 ATCA	
11801	12001	12101	12201	12301	1240	12501	12601	12701	12801	12901	1300.	1310.	1320.	13301	13401	13501	13601	13701	13801	1390	14001	

Fig. 38D

rHMPV-GFP (continued)

1000 1100 1400 1500 1600 1700 1900 2000 1200 1300 1800 2100 2200 2300 2400 2500 2600 2700 2800 3000 3100 3200 3300 3500 3600 2900 3400 700 800 900 300 400 200 900 TCCCGCAGAG CTAGTGGACA GACAAGTTAA ACCATGAACA TCGTTACTCA TTTGTGTGGA TGTTAGATAT CTAGAGACTA TATTTGAGCA GCTGAATTGA AATCAATAGA TATTCCAAGC ACAAGACACA CCCACAAAAC TATATTATG TATCGTTGGC CTAGATTTGC AATGATTGGT ATAGGTAATG CAAAAGAAAC GGTAAATGCA GAGTGAGTCA TCTGCAAGAG GGTACACCAA TAATGTTAGA CAACAGATTT GCTATTTTCT GTTCATGGGT AACACTATAT CCACCAAAAC TGAGCTTATT TGCTCTAAGA CTTGGTGTTG CAACCAATGA AATTAACAAG AATGCAGGGA GAACACTTC GATCTGTCAT GAGTTGCAAA CAGGTAACAT AGAAGTTGGA TTCTATGAAC TGTTTGTAAA AGCAGCAGAG ATGGGAAGAC GCTAGACTAG TCAGAGATGC AGATAACACT AGAAAGAGTA GTCTGTGCAA GCAGGACTGT AGAAGCTGCA GGAAAAAGTA AAGGTCAAAA CAAACACAGA AAGATATCCT AAAAGATGCC GAAGAAGAAC GGAGTCCTAT TGGTTTCCTC CAATACTCAA TCAGTTGGCA CAATCAAAGA CATGATCATG ATCAGCAGGA TAAAGATCAA TAACCAAAAG TGCAATAGCT GCTCTCAAAA TGACTAGTGC GTTTTCAGAC CAGATAAAAC ACTIGACTIT GATTATCATT AGAACAGGTT TCACCTAAGT TTGCAGCAAG CTCTAGGATC TAAAGGGGAA AAGGAATCAT CATCAACAAT AAGTCCAAAG GGAAGAGTGC ACGAAGAAAA CCTGAAGGAA CTATTGTAGG ATGGGCAGAC CCTTCCAGTG CCAAACTAGA AAGCATTGAG AGAGATGGAA AAATGAATCA TTTGACAATA AATACAGCAA TTGTCCTAGG TGCTAGATCT GCAGAAAGTT TAGGACATGT ATCAGAAGAA AAGTCAAGAT CAGAATGGTC TTCAGCCAAA AAGTCAGTTT AGCCGAGAGC CAGTGTTTTA AATCAAAGGT TTGTGCGGCA ATCTGCAGGA CAGGACTAAT TATATATCT GGAAAGTGAT GAACTTGACC AGCAAAAACC ACAATGGGAC TTCAAGGGAT ACCTTCATCA GTAAAAATAG GACTITGCIA ACTAAACTAG TACCGAAGAT ATCTAAGACA AATGTACAGA GGGCTCACAG GAAGATATCA AACGGCTGCA CAAGCGGTGA TACCAGCAAG AATTTGTGAG AAGTGAATGC ATTTGCACGG AGGAAGCAAA AACATAATGC AATGTCATTC CAAAATTGGC GGGAAATATA ATGGAAGAGG TGCTGCATCA GCACTTGATG AGCATTCATA GCACCCTATG CATATGTTCA AGAATTTGTG ACATGCCAAC AGAACCCAGT CATCATCACT AATAATTGCT AAAATGTCTT AAGGATATCT AATCAAAACA CAATCAAGGT TTCCTAAATG AAAATGTCTC CTGCAGTGAC GATACAATAT TTAGGGAAAG TTTAATATTC AGGGTAGATA CATCTTCAAC ATCATCTAAC GGGCTTTTAC GTATAATCGG GACAAGTCAA AGGTCACAAA ATAAAATAA GGGACAAGTA 9 AAACAATGGT CTCCTCATTA CTGCTAGAGC *FCAATGAAAA* AAATGAACCA GAGAGAGACA CAGCAGGACC AGCTGAAATG GACGAGAGCA ATGGTGTCAA CTTGAGAGTG CAACAGAAGA AAAGACTTAC CAACTCTGTA **IGCAACTGTG** TGACAATACC GAGCTAGGGG ACTATAACTG AAATCCCAGA GAGAGCTGAA AGCCAAAATT **IGTCCTAATC** GACCTAGCTT GGGACAAATA CAGAGATAGG GGCACCACAA GACATACTCT GAGGCAAGAA GTGTAGGTGC TCATTGCCAG TCAGGTCTAG AAAAAACTGG TAAAAAGATC ATCATCTACA GAAGAGGAAC CCTTCACATC AACCTTTGAA AACATTGCAA ATGTAGTTTA AATATACCTG CATTAACACA AACAAATTGA GCTTTAGGCT AGGGAAAAGC AATTGTTGAA TCTGGTAGAA TTGACAATAA TCGAAGTAAA ACCATATGGG AGTGATAGTA TAAAAATAAC TGTACTGATG AACCATAAGG ACCGCAGTAA AAGATACCCI TCCTGAATCT AAATCAACTI AATAGAAAGC ATCATGTAGI TCAGTCAAT AATTAAATTC CAAACAAAAC AAGAGATGTA TACTGATTAC AAATATGCTG TTCTAACCAA AATAGACAAA ATGCGCTCAA GTATGGGAAA AGGTGGGGTG GAGAAATGGG TCCTGTTGAA GCCGACCAAG GCGAGAGAAG ATTTTATTAT GAAAGCAACA CAGAAATCAC AACCTGCACG AACTTAATAA CCAGTTAATC TTCAAGTTGA CCTAGAGAAA AAATCTTACA TGGTAATGCT ATGAGTAATT AAGAAAGTTT CCTCAATCTT TCGTACACTT AAAGAAGCAA GCTAAAGACC CCCAAAAAAT CAACCATGAA CTGGAACACA AAAATCCAGA GGAAGGTATT ATTTAGAAGA CGATAGCCAA AGTCCTAGCC GCTGTCAGCT GGGTAGAAGA CACACCAATA GTGCTAAGTG ACACAATAAA GTTCAGGTGG TATTCATTGA AACAATGCTA GATTTGGTGA AAGCTTAAAA AGAAGCTTTC AAACAACAGA CAATGTAAAA AGAAATAATA AAGGCAAAAG GTGTTGTTCT CAAGATGATT ACCATCAGCA GACGCAGAGT TAGGACTGCT AAGATATTTA ACAGCTGCTG TGCTCGATCA AAGCAGTGAG AAACTAGGAG ACTTCATGGA GATATGTACT TTTAGAACTA AAGGAAAGTT GTGATGTTGA TGATCAGTTA GCAGGCATTG ATGGAGTGCG TCTGAAGATG GTCTGTACTT GTTTATTGA AACGCGTATA ACACTAAACA AGGCAGTGAA AATCAAGGAG AGCTAACAGA GAGTCTCAAT GAAAAGAGTT CAGCACCAGA TACAGGAGIC CAAAAATAGC CAAACAACCA GAGCCGGTCA AGAGGTTTAT GATTTTGCTA GTTATGCCAG TGATGACAAT AGAGCTACCT AATCTCCAAC TGAGGAAGAA AGCATGATAT AACTAATAGC ACTAACCGAG CATTCCCTAC TGTTAAAACA GCACTGTGTG AAGCTGCAAT TATATTCAAG CAAGGAACAA TATAAAAAA GCACGGACTA TTAGAAGTTG CAGTTTCTGC AGCAGTCACA ACACTAGGAA ACATTGCTGA CCAGCGGTTT GTGCTGCTAT HMPV strain ACGCGAAAAA TAAGAAATTC CAGTTAGAAG TATATTAAAA GAGATTCTTT ACATGGAGTG GAAAGTGTAT CAAGCTTATG AGCAAGTTAC GCAGCAGAAA TAAACATGAG AATGAAGCAG AAAAAATCAA TCTCAGACAA AGAGAAGCTA ATAAGAGAAG **TCAGGATAAC** CAGAGGCCTT CAATTGCCCC CACAGAAAAA GCAGTGTAAA CTTATCAAGG GCCACTGTTG ATTATAGTTA GAACTCAAAA CAACACACCA TCAGCTCAGG CGGTTTGCGA TGATCTAATT CTGGAGTCAC TGTCTTTACA CCACAGCAGC GGCAGTATCC AACAAATGTG CAGAAACTCT ATCCAAAAGG TAACACCTCA 401 2201 301 801 1001 1101 1201 1301 1401 1501 1601 1801 1901 2001 2101 2301 2401 2501 2601 2701 2801 2901 3001 3101 3201 3301 3501 501 601 701 901 701 3401 3601

GCTGTATCAT

GCTGGCCAGA

CTGATGCTGA

GACCTAATGA

AATATCATTG

TAACACCAGC

3701

GAACCGTGCA ATGG GAACCGTGCA ATGG ATGCAGGATC CACT ATCAAGAGAA TGCA AGGTTTGGTGG CACT CGATCCAATC AGGT AATCTGAACA AGGT CAATCAACAA AACA CAATCAACAA AACA ATAGCAATA ATGA AGAAGACAG ACTC CTACATAACA TATGA ACTACAACAA TATGA ACTACAACAA TAGA ATAGCAACAC GAAA GCTACAACAA TAGA ATAGAAACTC CTGG ACTGGAACACC CTGG GAGAAACTC CACA ACTGTCTAGC AGC TCCCACACAC CAGC ACTGGAACCC CTGG GACAACACC CTGG ACTGTCTCAC AGC TCCCACACAC CAGC TCCCACACAC CAGC TCCCACACAC CAGC CTCGAACCC CTGG GACAACACC CTGG GACAACACC CTGG GACAACACC CTGG GACAACACC CTGG GACAACACC CTGG CCTCGAACCC CTGG CCTCGAACCC CTGG GACCACACC CTGG CCTCGAACCC CAGA ACAATTGTT TGAG AAACAATTGTT TAAC TTAATTTTTAT AGAT AGAAACAATTGT TAAC TTAATTTTTAT AGAT
ACCGTGCA ATGGTGAGGA TACAGCTT GTTGGATAAT GCAGGATC CACTGTTTAC CAAGAGAA TGCAACATCA INTTGGAGA CTTGCTAACA INTTGAACA GTGCTAACA AATCAACA GTGCAAAAA AATCAACA TGCTAACAAAAAAAAAAAAAAAAAAAAAAAA

HMPV strain 75 (continued)

HMPV strain 75 (continued)

TGA 7900 TTA 8000 AAG 8100 TTT 8200 AGA 8300 TGT 8400 TGA 8500			ATT 10000 STA 10100 AAG 10200 AAG 10300 AAC 10400 ATT 10500	'пппппппппппппппппппппппппппппппппппп
	GATCAAAAAG GCAGGATGTT AACAAAGTAT GCAAGAGCCT CGCAAAGCTT	GATGTGAGTAT TAGATGAGT ATATATATCA ATAAATACAA TATTAAGGAA	TACAGATCTT AGATACGATT AGCTAAGGTA AATGAGAAG AGCTTGTCAA GCTTAGAGAAC TCTAAAGACAAC	CCAGGGCTAA CCAGGGCTAA CCAGGCATTA CCAAGCATTA ACTGGTAGAA TTGATAAAAT TGATCAGTTC GAACAGTGTG AAACCAAACT TTTTTGGAGA
TTAAGTCTAT CTAGGTTTAG TGATTACCCC TATTATATAT AGAGCTTAAC CAGGAATTTT	TIGCAAATIT TTAAGTGTAG CAGAAACTTT CAATTATATT TTACATGGCA	ATCCTTGTAN ACCTGAAGGTA AAGGTGAAAC AGGTCCCTGG GTTAGCTTGA	AGTAGTTITT AGTAGACTA CGGAAAGACA CTATAGCAGA AAGGCTGAAA TGTCTATGAT	GCACTCAGA GCACTCAGA TAAAGGAACT GTCCAATCAA AGAACAGTTA TATAAACTAG GTCAAAAACA AATATTAACA TGTGTATTTA TTGACAACACA TGTGTATTTA
TGATTATATG CAATTCAGTA TAGAAAACAA TGCAGAATTA CTTAAAACTGG TAAAAGTGCT ACAATTCGAA	ACTTAAAAGA AGAAAGAGAA CCCTTTTTCC ATAGTTACAA AGCAGATGAG	TGGAGGCGAT AGTAAAATTG AAACTCAAAG TATTAAGGGT AAGTATACTA CAATTGAACA	GGGGAGACCC CAATATTAAA GCGGTAGGAT GTGCTATTACA AACCTTTTCAT GATTGATATG	GTGGGGTGTA GGTGGGTGTA AAGATTTATG TTTGACACTA TGAGTGTTGT AAAATTCAAT ACTATAAAAG ATTGGTGTGG GATATTTCTA TTATTAAGAA CATTAGTAGGA
ATGAAACTGT TGAGCATGCT GGCACTATAT TAGAAAATGC TACAAAAATT ATTAAGAATT TTGCTGCAGTA	TAGAATTTT TAACTGGGAA TAATATTGTA AGGAAGAATG GCGCAGACGT	TTATGGACAA TCAGTAAACC CATTGGCCAT ATAAAAAGA TCAGAGGAGA	CAGTTTGGAG AAGTTTCAAA AGACCCCCAG TTTTGTGATA ATGAATCACT TCGAGGATATT TCGAGGATATT	AGCCCTTGG GGAAAATGC AAATTACCAC ATTAGTATAA TATTTCAAGG GCTTATGCCT CTTGCATGCCT CTTGCATGCCT AGATTTCAAA AAATTCCTAT
AATAAATTAT TTAAAATTAC TAGAGTTCTT AACAAGAATT ATAATGAGAT TTTTTAGAAC	GAGGAGAGA ATTGTCTCAT TTTTAGCTGA CATTAAAACT ACAGCTATCT	GTGTCAGAGG TCAATAGAAG CCTATAAAAA TCCTACCCC GAACTAGAGT	TATACCAATG TTACTGTTAA CACTAATGAG GAATCAGCTA AGAGTGCTCT CTATCAATGG	GGGGGCCAAA GGAAGCAATA TGTGTAAAAC ATAGGACAAC CAGCTGCGGA CCCCCTCCTG TAGGGAAGAT ATCTGCAGCA CATGCCTTCA TAGATGAATC ATATGATGTA
AGTGAAATTC AAAACAGATTC AAAACAGATC ATTATTAATT GTTAAATTAA TGTACAACAA	GICAAAGAAC CAAAGACCAC GCCGAGAAAC AACTITCITC ATATGAAACC	TTGAAGGGTG AGAATCAA ATAAGAGATG GGGTCATGCA TCTGTGTCAA CATCCGTTAG	TATGGATGAA CCATGTGGAT ACATTAACAA GTCTATCTCC TCACGGATTG AGAACATCTG	AGGGTCAGA AGGGTCAGA AGGGTCAGA GTTCCAGCTT AAAATGCAAT AGATATTAACAC TTGAATCTTT CATATCAGAT GAAGATATAAA GAAGATATAAA
ATCTACAAGG CTTTATTATG TGAAAGCTA AAAGTATAAA AATGGATGCT TTTGTAGATA TTTGAGCTAAG	ACCACATGA ACCTAAATGA ACAGATACTA ATGAAATCAG AAGCCTTTAG GACCACAATG	ATGGGGGGA TATTAAACGG GCTTAAAGAG CAATCTGAGG CAATAGGGAG GTCAAAACAG	GTGGTTGACC AAGCAATCAG TGAACGTGCT AGCATACTGA CTGTTTATCC CCTATTGCAG ATAATTAATA	CAGAGACCAA AAACAACAAA GTTTAGGTAT CCCAGCTTCC TAGAAGAGAT CAAAATTAAA GTGATGGGTT TGTAAAAGAT GTCAAAAAAA
TTTAGAAGTA AGTTCGAAGG ATTATCAATG GACGCTTTGA TATAAAAGGG CTTAGACG	AAACAAGAGT AAAGACAAAT AAAGACAAAT AATTATGGAA AAATTCAATC	CAGATACCAT ATGACCTCTC CAATTAAAAT TAAGGTGATT AGTGCAGAAT ACATGCATGA	AGAAATGAT TTCTTGACTG TAGAAAAGAA AGCAGTTACT AACATAACAC CTATAACTAA	TCAGTACTGA ACTTCTTCA TGCATAGGAA CCATGGAATT AGACATTAAT ATCCCCCAAT TTTCCATGGA AAAGACTGGG AAGGGAAAAA TGAATCAAAG
AGGACTAGGA CTAGTGAAAGA TTATTAGGG ATGTAGATG TACTAAGAAT CTTAAAAGTTAC	TTATGTAACT CCTGGCAACC ATCTCCAAAG AGACCTAAGT TTACATCTTA	GTGGGCTATA TCGTTGTCAG TATAGCTTAG AATTTATAAG CATTAAAACT TATAACTTAT	AGCIGAAGAA GACTCCTGAT TAAATAGAAC CATTGCAGAC GGTACAAAGT	
AAAATCAAGA AGGGTTCTCA TAAAATGGGT TAGTACTTAA TGGACACCCT GGAGCATTTA AAAAACCAAT	ACCTCAAACG TGCAATGCAA GGTGACTTGG CCATAGTAAC	GAAGAGCAAA CTGTTAAGAC AAAAGCAGAT AGAGATCTTC TACTAGATGA	AGALLITITG TTTACAGAG CTTTACAGAG CTTTACAGAG ACAGTGATA AAGTAGGGAT TATAGGTTGT	AGGAATATT GATCCTGTT GTTCCTGTT GTTATCTGTT AGTGAGAGGT GCCCAAACA AACCTCCGAT TTAAATAAGA TTAAATAAGA TTAAATAAGA
	(4 H 0 U 4	004417		, 4000464640

1900	2000	2100	2200	2300	2400	2500	2600	2700	2800	2900	3000	13100	13200	3280	
CAGACATGGC ACATGCTCTT ACACGATTAA TTAGGAAGAA ATTGATGTGT 11900	AGTIAITGAI CCIACAACAC AGCIAGACIA IIIICCIAAG GIAAIAITIG 12000	ACAAGAAATT ACATGACATT ATTACCATGG CAGCACGTAA ACAGGTATAA 12100	GGAAATTGAT AAAGGACTTA AACCCTAAGG TTCTTTACTT TATTGGAGAA 12200	ATTIGIATAT AGGAGITIAA AGGATGAICT IGAICACCAT TACCCATTAG 12300	GGATTATCAA TGGAGACCAC AGATGCAACT CAAAAGACTC ATTGGGACTT 12400	AATICAAAAA CAGAGAIGAI IICITIAAAA IGGIAAIICI IIGGAGAAAA 12500	ATTIGCAAAG TATCATGCGA CGGACTGCAA TATAAAGTTA CCATTITITG 12600	GAATGITACA TACTITIAAC ATTAGGICAT CACAATAATC IGCCAIGICA 12700	ATGCCTCAAA AAAACTAGAC AACAAATCAA TTGAAGCAAA CTGCAAATCT 12800	AAAGAAACTG TTAACACTAC AAAGCAATCA TTCTTCCATA GCAACAGTTG 12900	ATAATIGAIT GGITAGAGCA TATCTIGAAT ICTCCAAGAG GIGAATTAAA 13000		ATTA 1	~	100
ATTGAT	GTAATA	ACAGGT	TATTGG	TACCCA	ATTGGG	TTGGAG	CCATIT	TGCCAT	CTGCAA	GCAACA	GTGAAT	CAAAGT	TTGACC		
AAGAA	CTAAG	CGTAA	TACIT	ACCAT	GACTC	ATTCT	AGTTA	TAATC	GCAAA	CCATA	PAGAG	TTATAGATAA CCTGGGAAAT GCAGAGATAA AAAAACTAAT CAAAGTTACC	AATCTCACAC AACTGAGAAA ATGATCATCT AACAGTTTAA TTGACCATTA		90
TTAGG	TTTT	CAGCA	TTCTI	TGATO	CAAA	TGGT	TATA	CACA	TTGA	TTCTI	TCTCC	AAAAA	AACAG		
ATTAA	GACTA	CATGG	TAAGG	GATCT	CAACT	TAAAA	TGCAA	GTCAT	ATCAA	AATCA	TGAAT	GATAA	CATCT	GCCGT	8.0
ACACG	AGCTA	ATTAC	AACCC	AGGAT	AGATO	TTCTT	CGGAC	ATTAG	AACA	AAAGC	TATCI	GCAGA	ATGAT	TTTT	
SCTCTT	SACAC	SACATT	SACTTA	STTTAA	BACCAC	SATGAT	ATGCGA	LTTAAC	TAGAC	CACTAC	AGAGCA	SGAAAT	SAGAAA	GAAATTGAAT GTATACGGTT TTTTTGCCGT	70
ACATO	CCTAC	ACATO	AAAGG	AGGAC	TGGAC	CAGAC	TATC	TACT	AAAAC	TTAAC	GGTT?	CCTGC	AACTC	GTAT2	
CATGGC	ATTGAT	SAAATT	ATTGAT	STATAT	LATCAA	CAAAAA	SCAAAG	STTACA	CTCAAA	AAACTG	LTGATT	AGATAA	CACAC	ITGAAT	09
CAGAC	AGTT	ACAAC	GGAA	ATTT(GGAT	AATT(ATTT	GAAT	ATGC	AAAG)	ATAA	TTAT/	AATC	GAAA.	
TTATA	ACTCA	AGTTA	CATCG	ATAAA	GTGAA	TGCAG	TACT	GATCA	TTTCC	AGACA	GTACA	CAAGC	ACCAT	AAATT	50
TTGAA	GTCTA	AGGGA	ACATG	CTGAC	TGGTG	TGTGA	ATCTI	GTCAG	AATGA	TAAAT	AGCAA	ATGAT	AATCA	ATAAG	
ACTGIT	GTTTA	ACTACAACAA AGGGAAGTTA	LTGAAG	AGTATC	AATAGA	ACATTG	SAACAG	CAAATT	STGTGT	AAGAGT	TAAAGAATAA AGCAAGTACA	CCCAAT	AATAAT	LAAAAA	4
AATAA	CCAA	ACTAC	CAGC	TGTG/	GAGT	GATA	TATG	GAAG	AGCAC	AAAA	TAAAC	ATAT	TAAT	TTGA	
TTTAAG	TCATCA	GTTCAG	TAAAAT	ACAGCA	TAAATA	TTTATT	ACAGCT	TGCAAG	GAGAAT	ATAAAC	AATGGT	GAACAC	TAATAA	AACTAA	_
TATC	AAGT	ACCA	GATG	AAGA	GATT	, ATGC	CTGT	. ATTA	AAAT	. ACCA	TCCA	TAGA	GAAG.	TAGT	
AAAGTO	TAATCC	TATGAC	CAACAC	GATGGC	ATAGGI	GTAAAG	TAGAAT	ACTTT	ATTCC/	AAGAAT	ATAGA	AAGCA1	GAGTG	ATAAAT	00 1
GAAG	TCTT	AAGT	AGTT	ACTG	GGTA	ATAA	CATG	7 AGCT	CAAA	GATT	GATT	TTTG	TIGI	AATT	_
TTAATA	ATGCAC	GTTAAA	GICILI	CAGGIZ	TCAAAG	CACAG	TATTAT	GTCTG1	GAAAT	TATCAC	AAGTA	GATTIC	ATATGO	ATTAA	-
11801 GCAGTTAATA GAACAAAGTC TATCTTTAAG AATAACTGTT TTGAATTATA	11901 GATAATGCAC TCTTTAATCC AAGTTCATCA CCAATGTTTA GTCTAACTCA	12001 AAAGGTTAAA AAGTTATGAC ACCAGTTCAG	12101 TITIGICITI AGTICAACAG GAIGTAAAAT CAGCTIGAAG ACAIGCAICG	12201 GGAGCAGGTA ACTGGATGGC AAGAACAGCA TGTGAGTATC CTGACATAAA	12301 AATATCAAAG GGTAATAGGT GATTTAAATA GAGTAATAGA TGGTGGTGAA	12401 GATACACAGA ATAAGTAAAG ATGCTTTATT GATAACATTG TGTGATGCAG	12501 CATGTATTAT CATGTAGAAT CTGTACAGCT TATGGAACAG ATCTTTACTT	12601 TAAGGTCTGT AGCTACTTTT ATTATGCAAG GAAGCAAATT GTCAGGATCA	12701 CGGAGAAATA CAAAATTCCA AAATGAGAAT AGCAGTGTGT AATGATTTCC	12801 CTTCTATCAG GATTAAGAAT ACCAATAAAC AAAAAAGAGT TAAATAGACA	12901 GCGGAAGTAA GATTATAGAA TCCAAATGGT	13001 CTATGATTTC TTTGAAGCAT TAGAGAACAC ATATCCCAAT ATGATCAAGC	13101 GGGTATATGC TTGTGAGTGA GAAGTAATAA TAATAATAAT AATCAACCAT	13201 GTTAATTAAA AATTATAAAT TAGTAACTAA TTGATAAAAA ATAAGAAATT	
11801	11901	12001	12101	12201	12301	12401	12501	12601	12701	12801	12901	13001	13101	13201	